Towards a Useful and Usable Bioinformatics Infrastructure

Terence Critchlow

Center for Applied Scientific Computing
Lawrence Livermore National Laboratory
www.llnl.gov/CASC/people/critchlow

Georgia Tech Department of Computer Science



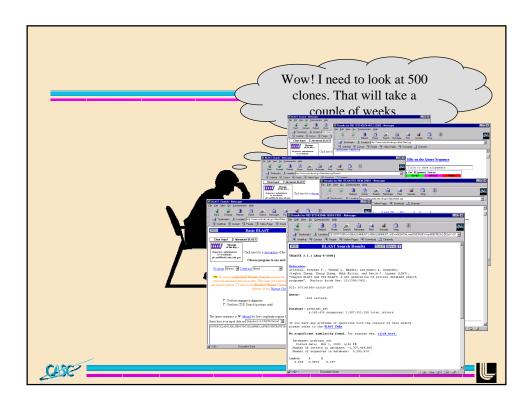


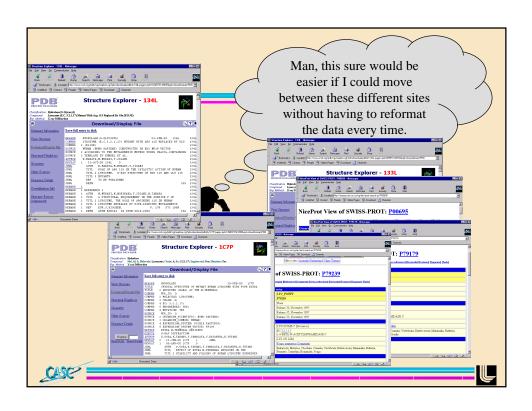
Outline

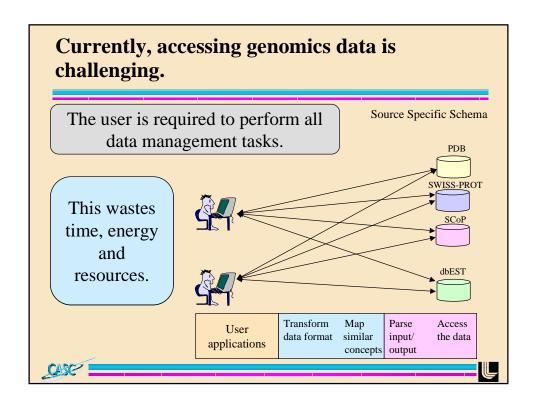
- A day in the life of a geneticist/biologist.
- CS to the rescue! (well, maybe....)
- DataFoundry's meta-data infrastructure.
- Future research directions.

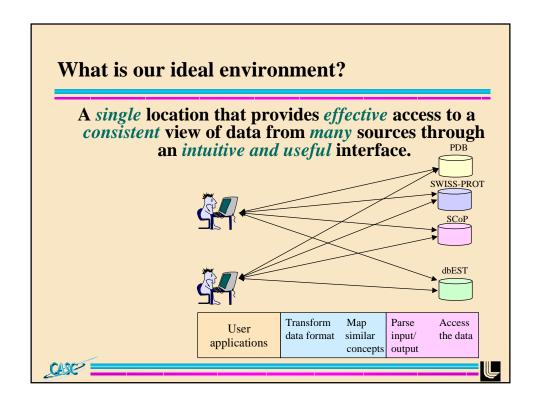


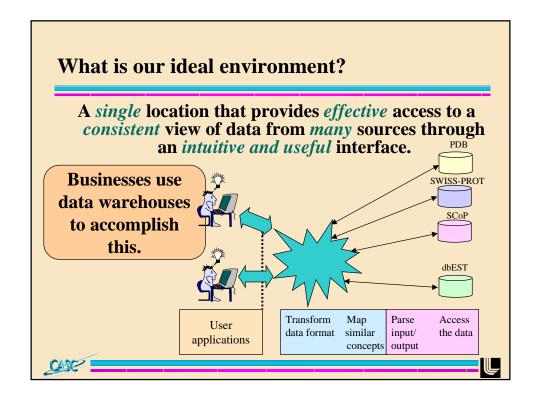


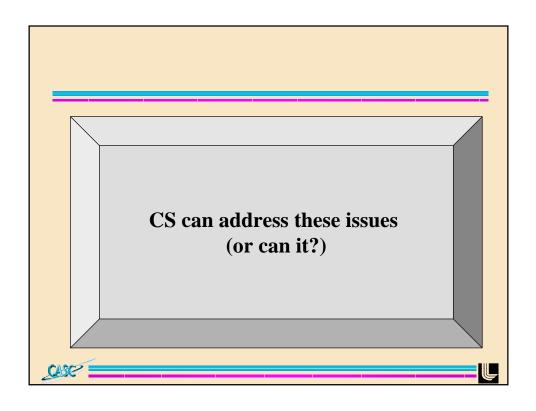


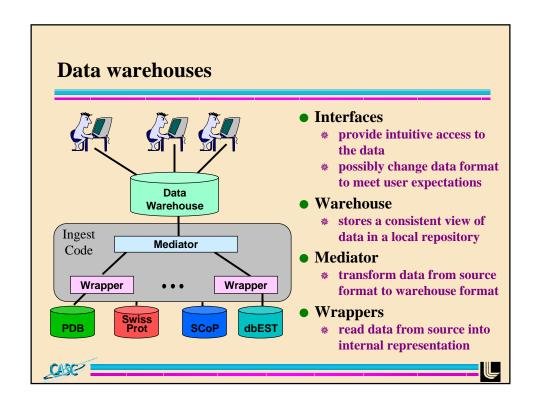


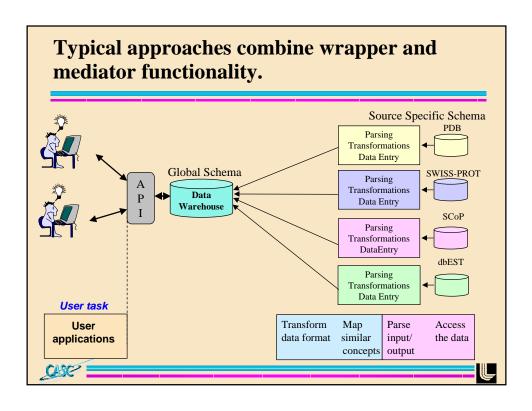


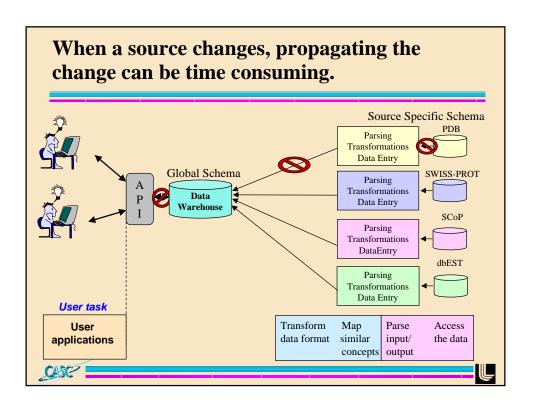


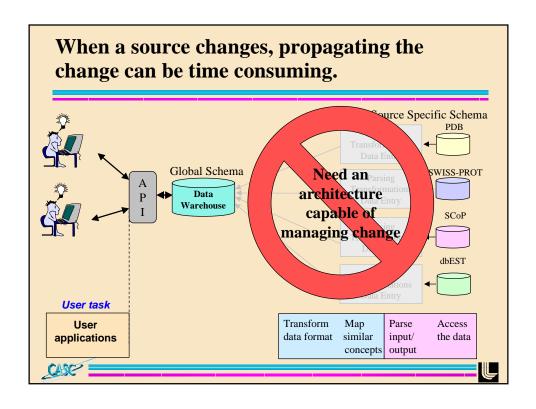


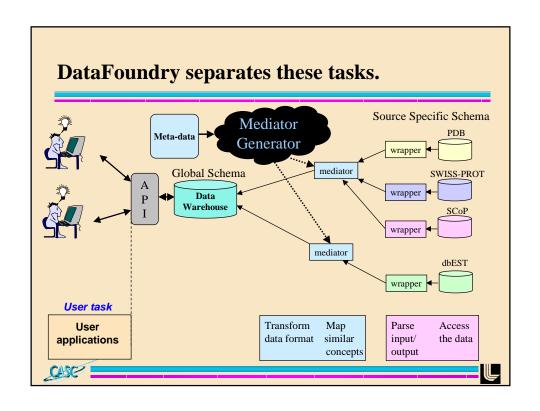


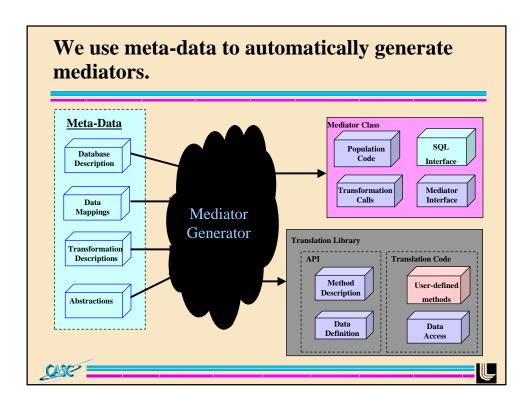


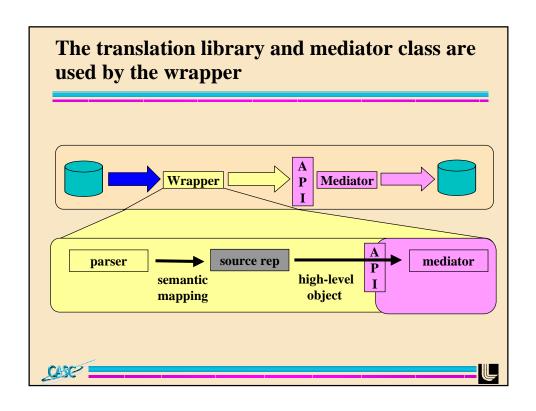


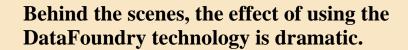










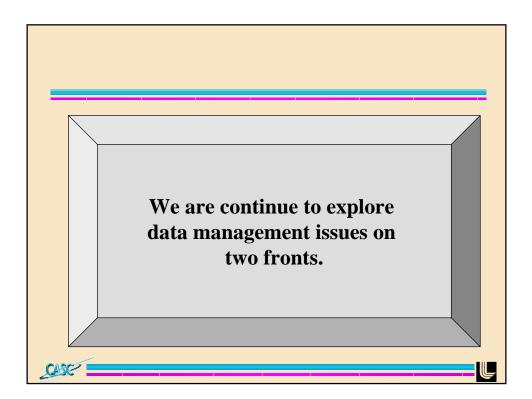


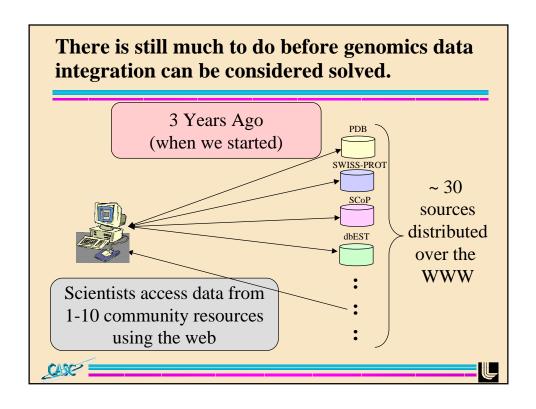
Cost of integrating SCoP into warehouse that already contains PDB and SWISS-PROT.

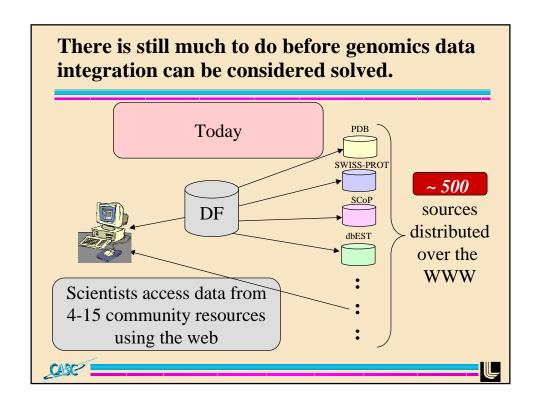
Activity/ integration style	typical	DataFoundry	diff	%diff
understanding SCOP	2.0	2.0	0.0	0
writing wrapper	4.5	2.5	2.0	44%
modifying schema	0.5	0.5	0.0	0
writing mediator	4.0	0.0	4.0	
modifying meta-data	0.0	1.0	(1.0)	
total time in days	11.0	6.0	5.0	45%

DataFoundry makes it possible to build and maintain scientific data warehouses.









There are several challenges to querying hundreds of sources:

- Usable descriptions of relevant interfaces
 - query input/output descriptions required
- Automatic creation of wrappers
 - human interaction infeasible
- Intuitive presentation of non-integrated data
 - semantic integration of data too difficult
- Selective querying of data sources
 - data source categorization needed



